

# Gene Cart

## Introduction

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Home > Analysis Cart > Genes

## Gene Cart

**Gene Cart** is a way to save interested genes in IMG for continuing studies, as shown in Figure 1.

Gene Cart

Gene List

Upload & Export

Comparison Tools

Chromosome Map

Sequence Alignment

Gene Neighborhoods

Profile and Alignment Tools

Genome Filter

Gene Profile

Occurrence Profile

Function Alignment

Gene List

4 gene(s) in cart

Remove Selected Add Scaffolds of Selected Genes to Cart Select All Clear All

Toggle Selected

4 of 4 rows selected

Search column: Gene Product Name Search term:

Export Page 1 of 1 << first < prev 1 next > last >> All

Column Selector Select Page Deselect Page

Selection	Gene Object ID	Locus Tag	Gene Product Name	AA Sequence Length (aa)	Genome	Batch <sup>1</sup>	Scaffold External Accession	Scaffold Length (bp)	Contig GC %	Contig Read Depth
<input checked="" type="checkbox"/>	<a href="#">637020907</a>	0q_2177	shikimate kinase (EC 2.7.1.71) (MGterm)	168	<a href="#">Aquifex aeolicus VF5</a>	1	NC_000918	1551335	0.43	
<input checked="" type="checkbox"/>	<a href="#">637024562</a>	CPn1038	shikimate kinase (EC 2.7.1.71) (MGterm)	176	<a href="#">Chlamydomonas reinhardtii CRL029</a>	1	NC_000922	1230230	0.41	
<input checked="" type="checkbox"/>	<a href="#">637004723</a>	CT367	shikimate kinase (EC 2.7.1.71) (MGterm)	184	<a href="#">Chlamydia trachomatis</a>	1	NC_000117	1042519	0.41	

Figure 1: Gene Cart.

The default columns displayed in Gene Cart table are “Gene Object ID”, “Locus Tag”, “Gene Project Name”, “AA Sequence Length”, “Genome”, “Batch”, “Scaffold External Accession”, “Scaffold Length”, “Contig QC %” and “Contig Read Depth”.

In IMG 3.3, Gene Cart table is added with the functionality of **Table Configuration**, as shown in Figure 2.

### Table Configuration

**Additional Output Columns**

Expand All
Collapse All

<div style="margin-bottom: 5px;"> <input type="checkbox"/> <b>Gene Field</b> </div> <ul style="list-style-type: none"> <li><input type="checkbox"/> Gene Symbol</li> <li><input type="checkbox"/> GenBank Accession</li> <li><input type="checkbox"/> Chromosome</li> <li><input type="checkbox"/> Start Coord</li> <li><input type="checkbox"/> End Coord</li> <li><input type="checkbox"/> Strand</li> <li><input type="checkbox"/> DNA Sequence Length</li> <li><input type="checkbox"/> Locus Type</li> <li><input type="checkbox"/> Is Pseudogene</li> <li><input type="checkbox"/> Is Obsolete</li> <li><input type="checkbox"/> Add Date</li> </ul>	<div style="margin-bottom: 5px;"> <input checked="" type="checkbox"/> <b>Scaffold/Contig Field</b> </div> <ul style="list-style-type: none"> <li><input type="checkbox"/> Scaffold Object ID</li> <li><input checked="" type="checkbox"/> Scaffold External Accession</li> <li><input type="checkbox"/> Scaffold Name</li> <li><input checked="" type="checkbox"/> Scaffold Length</li> <li><input checked="" type="checkbox"/> Contig GC %</li> <li><input checked="" type="checkbox"/> Contig Read Depth</li> </ul>	<div style="margin-bottom: 5px;"> <input type="checkbox"/> <b>Function Category</b> </div> <ul style="list-style-type: none"> <li><input type="checkbox"/> COG ID and Name</li> <li><input type="checkbox"/> Pfam ID and Name</li> <li><input type="checkbox"/> KEGG Orthology ID, Name and Definition</li> </ul>
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Display Genes Again
Select All
Clear All

Figure 2: Table Configuration.

The **Table Configuration** selector lists three groups of “Additional Output Columns”:

1. Gene Field:  
Gene Symbol; GenBank Accession; Chromosome; Start Coord; End Coord; Strand; DNA Sequence Length; Locus Type; Is Pseudogene; Is Obsolete; Add Date
2. Scaffold/Contig Field:  
Scaffold Object ID; Scaffold External Accession; Scaffold Name; Scaffold Length; Contig GC %; Contig Read Depth
3. Function Category:  
COG ID and Name; Pfam ID and Name; KEGG Orthology ID, Name and Definition

User can use “Expand All” and “Collapse All” buttons to show or hide these columns, or click on the top “+/-” symbols to display or hide columns in each group.

To select/deselect columns in **Table Configuration** selector, user simply needs to select/deselect the checkbox next to the column name. Or user can click on the checkbox next to the top group name, to select/deselect the whole group. The “Select All” and “Clear All” buttons at the bottom are provided to facilitate such selections/de-selections. After choosing the desire columns, user needs to click the “Display Genomes Again” button to display.

Further, in IMG 3.3, the “Add to Function Cart” button also has the capability to add “GO”, “InterPro” and “Transporter Classification” into the Function Cart, as shown in Figure 3.

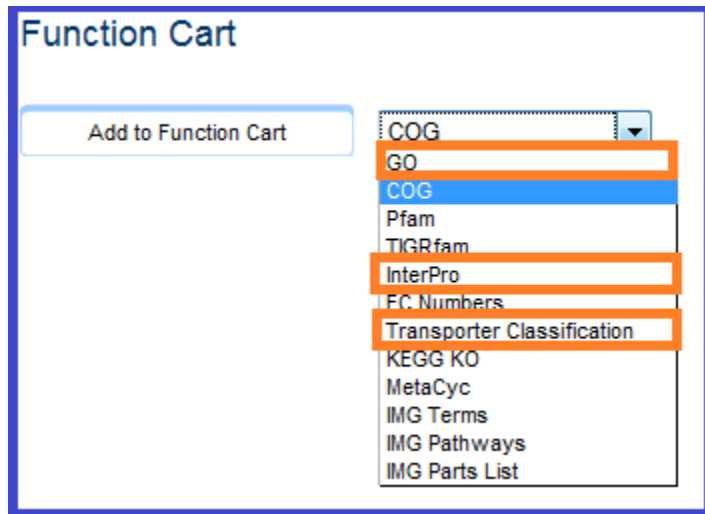


Figure 3: GO, InterPro and Transporter Classification in “Add to Function Cart”.